

# Structure of NHELP1 and alignment of Na\_H\_Exchange motifs

FIG. 1A

NHELP1(645 a.a.)



FIG. 1B

Na\_H\_Exchange motif

consensus	1	ILLLIILLVLA	10	20	30	40	50	60
NHELP	18	hggavellvfnflliltlti	20	30	40	50	60	77
gi 3877723	50	VSMVLIVVTAWAFKHYRFRf	60	70	80	90	100	106
gi 3319946	5	VILRYGTPATSGRDKSLCTqedr	10	20	30	40	50	59
gi 6919937	78	ILLTLTILTILWLFKHRRARf	80	90	100	110	120	132



**Na H Exchanger motif (continued)**

10050998, 013002

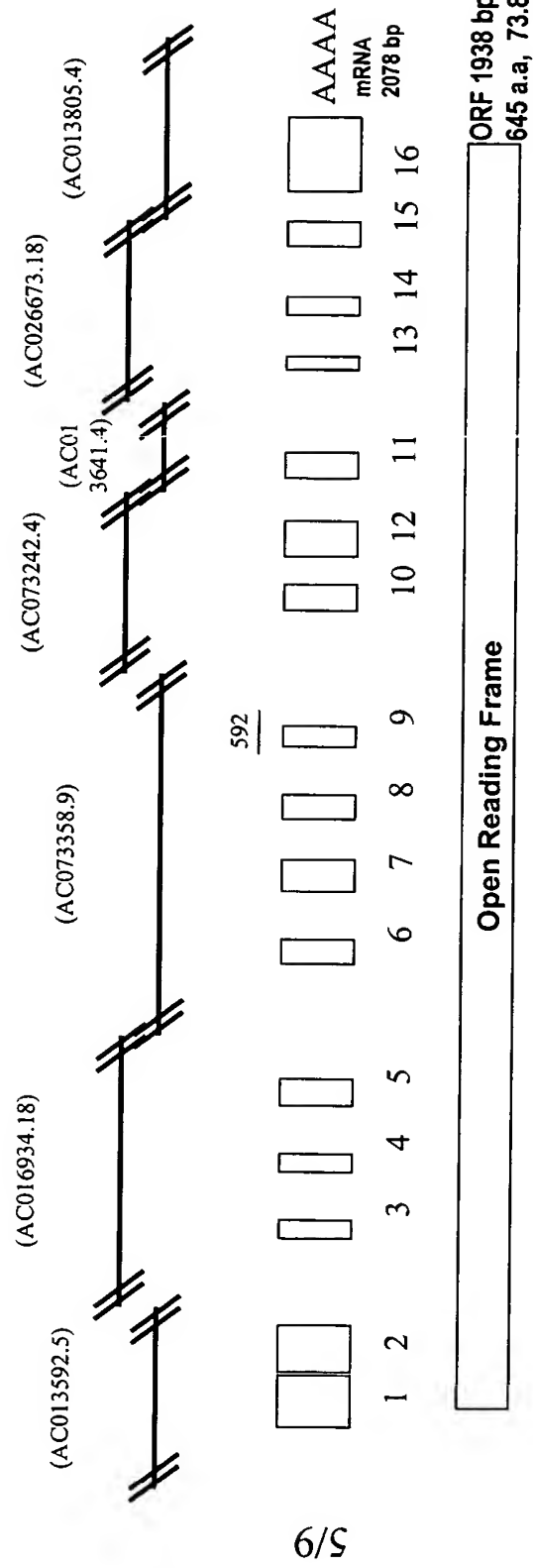
# **FIG. 1B**

## **Na<sub>H</sub> Exchanger motif (continued)**

		430	440	450	460	470	480
		..... ..... ..... ..... ..... ..... .....					
consensus	331	REKIPFGDQLVIGWGGLRGAV	ALALSGPLTSGPARDLILTT	AIIVVLVTVLVQG	ITLK	390	
NHELP	424	KQKIPWNFQHMMMFSGLRGA	IAFALAIRNTESqpkqmmf	ttlllvfftvvvfgggt	tpm	483	
gi 3877723	444	RPKIPKRYQHMLFAGLRGA	MAFALAGRNTSTENRQ	--MIFATTAVVIVTVLVN	GGLTS	501	
gi 3319946	363	RHKIGWNFQHMMMFSGLR	GAFAAIRDTASYARQ	--MMFTTLLIIVFFTVWI	IIGGTT	420	
gi 6919937	441	RSKIGSNFQHMMMFAGLR	GAFAAIRDTATYARQ	--MMFSTTLLIIVFFTVV	VFGGTT	498	

		490
		.....
consensus	391	PLVKKLRVKE 400
NHELP	484	ltwlqirvgv 493
gi 3877723	502	WMIDYLQIKH 511
gi 3319946	421	PMLSWLNIRV 430
gi 6919937	499	AMLSCLHIRV 508

# Structure of the NHELP1 gene (Chr. 3q23)



**FIG. 2**

10060998.013000

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## NHELP1

nt: SEQ ID NO: 1

aa: SEQ ID NO: 3

atagcccttatccagggtttttatctaaggaatcccaagaagactgggga												49	
M	E	R	Q	S	R	V	M	S	E	K	D	E	13
ATG	GAG	AGA	CAG	TCA	AGG	GTT	ATG	TCA	GAA	AAG	GAT	GAG	88
Y	Q	F	Q	H	Q	G	A	V	E	L	L	V	26
TAT	CAG	TTT	CAA	CAT	CAG	GGA	GCG	GTG	GAG	CTG	CTT	GTC	127
F	N	F	L	L	I	L	T	I	L	T	I	W	39
TTC	AAT	TTT	TTG	CTC	ATC	CTT	ACC	ATT	TTG	ACA	ATC	TGG	166
L	F	K	N	H	R	F	R	F	L	H	E	T	52
TTA	TTT	AAA	AAT	CAT	CGA	TTC	CGC	TTC	TTG	CAT	GAA	ACT	205
G	G	A	M	V	Y	G	L	I	M	G	L	I	65
GGA	GGA	GCA	ATG	GTG	TAT	GGC	CTT	ATA	ATG	GGA	CTA	ATT	244
L	R	Y	A	T	A	P	T	D	I	E	S	G	78
TTA	CGA	TAT	GCT	ACA	GCA	CCA	ACT	GAT	ATT	GAA	AGT	GGA	283
T	V	Y	D	C	V	K	L	T	F	S	P	S	91
ACT	GTC	TAT	GAC	TGT	GTA	AAA	CTA	ACT	TTC	AGT	CCA	TCA	322
T	L	L	V	N	I	T	D	Q	V	Y	E	Y	104
ACT	CTG	CTG	GTT	AAT	ATC	ACT	GAC	CAA	GTT	TAT	GAA	TAT	361
K	Y	K	R	E	I	S	Q	H	N	I	N	P	117
AAA	TAC	AAA	AGA	GAA	ATA	AGT	CAG	CAC	AAC	ATC	AAT	CCT	400
H	Q	G	N	A	I	L	E	K	M	T	F	D	130
CAT	CAA	GGA	AAT	GCT	ATA	CTT	GAA	AAG	ATG	ACA	TTT	GAT	439

Fig. 3

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P	E	I	F	F	N	V	L	L	P	P	I	I	143
CCA	GAA	ATC	TTC	TTC	AAT	GTT	TTA	CTG	CCA	CCA	ATT	ATA	478
F	H	A	G	Y	S	L	K	K	R	H	F	F	156
TTT	CAT	GCA	GGA	TAT	AGT	CTA	AAG	AAG	AGA	CAC	TTT	TTT	517
Q	N	L	G	S	I	L	T	Y	A	F	L	G	169
CAA	AAC	TTA	GGA	TCT	ATT	TTA	ACG	TAT	GCC	TTC	TTG	GGA	556
T	A	I	S	C	I	V	I	G	L	I	M	Y	182
ACT	GCC	ATC	TCC	TGC	ATC	GTC	ATA	GGG	TTA	ATT	ATG	TAT	595
G	F	V	K	A	M	I	H	A	G	Q	L	K	195
GGT	TTT	GTG	AAG	GCT	ATG	ATA	CAT	GCT	GGC	CAG	CTG	AAA	634
N	G	D	F	H	F	T	D	C	L	F	F	G	208
AAT	GGA	GAC	TTT	CAT	TTC	ACT	GAC	TGT	TTA	TTT	TTT	GGT	673
S	L	M	S	A	T	D	P	V	T	V	L	A	221
TCA	CTG	ATG	TCT	GCT	ACA	GAT	CCA	GTG	ACA	GTG	CTG	GCC	712
I	F	H	E	L	H	V	D	P	D	L	Y	T	234
ATT	TTC	CAT	GAA	CTG	CAC	GTC	GAC	CCT	GAC	CTG	TAC	ACA	751
L	L	F	G	E	S	V	L	N	D	A	V	A	247
CTC	TTG	TTT	GGA	GAG	AGT	GTG	TTG	AAT	GAT	GCA	GTG	GCC	790
I	V	L	T	Y	S	I	S	I	Y	S	P	K	260
ATA	GTC	CTT	ACA	TAT	TCT	ATA	TCC	ATT	TAC	AGT	CCC	AAG	829
E	N	P	N	A	F	D	A	A	A	F	F	Q	273
GAG	AAT	CCA	AAT	GCA	TTT	GAT	GCC	GCA	GCA	TTC	TTC	CAG	868
S	V	G	N	F	L	G	I	F	A	G	S	F	286
TCT	GTG	GGG	AAT	TTC	CTG	GGA	ATC	TTC	GCT	GGC	TCA	TTT	907
A	M	G	S	A	Y	A	I	I	T	A	L	L	299
GCA	ATG	GGG	TCT	GCG	TAT	GCC	ATC	ATC	ACA	GCA	CTG	TTG	946
T	K	F	T	K	L	C	E	F	P	M	L	E	312
ACC	AAA	TTT	ACC	AAG	CTG	TGT	GAG	TTC	CCG	ATG	CTG	GAA	985

Fig. 3

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T	G	L	F	F	L	L	S	W	S	A	F	L	325
ACC	GGC	CTG	TTT	TTC	CTG	CTT	TCT	TGG	AGT	GCC	TTC	CTG	1024
S	A	E	A	A	G	L	T	G	I	V	A	V	338
TCT	GCC	GAG	GCT	GCC	GGC	CTA	ACA	GGG	ATA	GTT	GCT	GTT	1063
L	F	C	G	V	T	Q	A	H	Y	T	Y	N	351
CTC	TTC	TGT	GGA	GTC	ACA	CAA	GCA	CAT	TAT	ACC	TAC	AAC	1102
N	L	S	S	D	S	K	I	R	T	K	Q	L	364
AAT	CTG	TCT	TCG	GAT	TCC	AAA	ATA	AGA	ACT	AAA	CAG	TTG	1141
F	E	F	M	N	F	L	A	E	N	V	I	F	377
TTT	GAA	TTT	ATG	AAC	TTT	TTG	GCG	GAG	AAC	GTC	ATC	TTC	1180
C	Y	M	G	L	A	L	F	T	F	Q	N	H	390
TGT	TAC	ATG	GGC	CTG	GCA	CTG	TTC	ACG	TTC	CAG	AAT	CAT	1219
I	F	N	A	L	F	I	L	G	A	F	L	A	403
ATC	TTT	AAT	GCT	CTT	TTT	ATA	CTT	GGA	GCC	TTT	CTA	GCA	1258
I	F	V	A	R	A	C	N	I	Y	P	L	S	416
ATT	TTT	GTT	GCC	AGA	GCC	TGC	AAC	ATA	TAT	CCC	CTC	TCC	1297
F	L	L	N	L	G	R	K	Q	K	I	P	W	429
TTC	CTC	CTG	AAT	CTA	GGC	CGA	AAA	CAG	AAG	ATC	CCC	TGG	1336
N	F	Q	H	M	M	M	F	S	G	L	R	G	442
AAC	TTT	CAG	CAC	ATG	ATG	ATG	TTT	TCA	GGT	TTG	CGA	GGA	1375
A	I	A	F	A	L	A	I	R	N	T	E	S	455
GCG	ATC	GCA	TTT	GCC	TTA	GCT	ATT	CGG	AAC	ACA	GAA	TCT	1414
Q	P	K	Q	M	M	F	T	T	T	L	L	L	468
CAG	CCC	AAA	CAA	ATG	ATG	TTT	ACC	ACT	ACG	CTG	CTC	CTC	1453
V	F	F	T	V	W	V	F	G	G	G	T	T	481
GTG	TTC	TTC	ACT	GTC	TGG	GTA	TTT	GGA	GGA	GGA	ACA	ACC	1492
P	M	L	T	W	L	Q	I	R	V	G	V	D	494
CCC	ATG	TTG	ACT	TGG	CTT	CAG	ATC	AGA	GTT	GGC	GTG	GAC	1531

Fig. 3



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L	D	E	N	L	K	E	D	P	S	S	Q	H	507
CTG	GAT	GAA	AAT	CTG	AAG	GAG	GAC	CCC	TCC	TCA	CAA	CAC	1570
Q	E	A	N	N	L	D	K	N	M	T	K	A	520
CAG	GAA	GCA	AAT	AAC	TTG	GAT	AAA	AAC	ATG	ACG	AAA	GCA	1609
E	S	A	R	L	F	R	M	W	Y	S	F	D	533
GAG	AGT	GCT	CGG	CTC	TTC	AGA	ATG	TGG	TAT	AGC	TTT	GAC	1648
H	K	Y	L	K	P	I	L	T	H	S	G	P	546
CAC	AAG	TAT	CTG	AAA	CCA	ATT	TTA	ACC	CAC	TCT	GGT	CCT	1687
P	L	T	T	T	L	P	E	W	C	G	P	I	559
CCG	CTG	ACT	ACA	ACA	TTA	CCT	GAA	TGG	TGT	GGT	CCG	ATT	1726
S	R	L	L	T	S	P	Q	A	Y	G	E	Q	572
TCC	AGG	CTG	CTT	ACC	AGT	CCT	CAA	GCC	TAT	GGG	GAA	CAG	1765
L	K	E	D	D	V	E	C	I	V	N	Q	D	585
CTA	AAA	GAG	GAT	GAT	GTG	GAA	TGC	ATT	GTA	AAC	CAG	GAT	1804
E	L	A	I	N	Y	Q	E	Q	A	S	S	P	598
GAA	CTA	GCC	ATA	AAT	TAC	CAG	GAG	CAA	GCC	TCC	TCA	CCC	1843
C	S	P	P	A	R	L	G	L	D	Q	K	A	611
TGC	AGT	CCT	CCT	GCA	AGG	CTA	GGT	CTG	GAC	CAG	AAA	GCT	1882
S	P	Q	T	P	G	K	E	N	I	Y	E	G	624
TCA	CCC	CAG	ACG	CCA	GGC	AAG	GAA	AAC	ATT	TAT	GAG	GGA	1921
D	L	G	L	G	G	Y	E	L	K	L	E	Q	637
GAC	CTC	GGC	CTG	GGA	GGC	TAT	GAA	CTC	AAG	CTT	GAG	CAA	1960
T	L	G	Q	S	Q	L	N	*					646
ACT	TTG	GGT	CAA	TCC	CAG	TTG	AAT	TAA	ttggcatgaagagta				2002
cagatgtaatcacaagtaatgcaagactcactgaggaataacaagccaagctg													2054
atgaggcagtacaggggagaggct													2078

Fig. 3